

University of Groningen

Data-driven Modelling of Intrinsically Disordered Proteins

Tamiola, Kamil

DOI:
[10.33612/diss.96266373](https://doi.org/10.33612/diss.96266373)

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2019

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):
Tamiola, K. (2019). *Data-driven Modelling of Intrinsically Disordered Proteins*. [Thesis fully internal (DIV), University of Groningen]. University of Groningen. <https://doi.org/10.33612/diss.96266373>

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment>.

Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

Propositions
accompanying the thesis

Data-driven Modelling of Intrinsically Disordered Proteins

by
Kamil Tamiola

1. Chemical shifts of intrinsically disordered proteins can be predicted from their amino acid sequences. — Chapter 2
2. Chemical shift libraries compiled from chemically unfolded and short—length polypeptides are not representative of intrinsically disordered states. — Chapter 2
3. The 'random—coil' term does not reflect the conformational preferences of peptide chains and should be used with great care. — Chapter 6
4. Numerical simulations based on experimental observations can be of fundamental importance for drawing inferences of how biochemical systems are organized, function, and are regulated.
5. Data—driven automation is the future of structural biochemistry.
6. Academic excellence is a multi—modal function of creativity, stubbornness and luck.
7. Open--access publishing and citizen science projects may avert the damage done by institutionalized pseudo—science and 'fake news' movements.